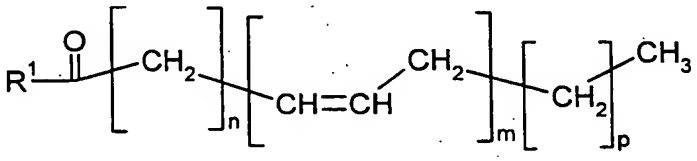
We claim:

1. A process for the production of compounds of the general formula I



(I)

in the seed of transgenic plants with a content of at least 20% by weight based on the total lipid content, which comprises the following process steps:

a) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ9-elongase and Δ6-desaturase activity, and

b) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ8-desaturase and Δ6-elongase activity, and

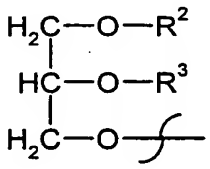
c) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ5-desaturase activity, and

d) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ5-elongase activity, and

e) introducing, into the organism, at least one nucleic acid sequence which encodes a Δ4-desaturase activity, and

where the variables and substituents in formula I have the following meanings:

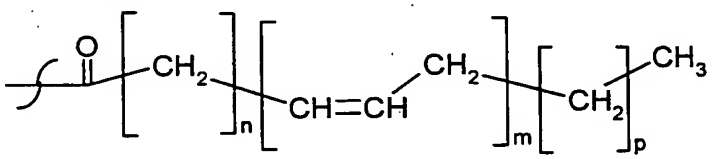
R^1 = hydroxyl, coenzyme A (thioester), lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lyso-diphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol, sphingo base or a radical of the general formula II



(II)

R^2 = hydrogen, lysophosphatidylcholine, lysophosphatidylethanolamine, lysophosphatidylglycerol, lysodiphosphatidylglycerol, lysophosphatidylserine, lysophosphatidylinositol or saturated or unsaturated C_2-C_{24}-alkylcarbonyl,

R^3 = hydrogen, saturated or unsaturated C_2-C_{24}-alkylcarbonyl, or R^2 and R^3 independently of one another are a radical of the general formula Ia:



(Ia)

in which

n = 2, 3, 4, 5, 6, 7 or 9, m = 2, 3, 4, 5 or 6 and p = 0 or 3.

2. The process according to claim 1, wherein the variables n, m and p have the following meanings:

n = 2, 3 or 5, m = 4, 5 or 6 and p = 0 or 3.

3. The process according to claim 1 or 2, wherein, in formula I, m = 4, n = 3, p = 3 and the compound is arachidonic acid and/or m = 5, n = 3, p = 0 and the compound is eicosapentaenoic acid and/or m = 5, n = 5, p = 0 and the compound is docosapentaenoic acid and/or m = 6, n = 3, p = 0 and the compound is docosahexaenoic acid.

4. The process according to claims 2 to 3, wherein, in the seed of the transgenic plant, the content of all compounds of the formula I together amounts to at least 27% by weight based on the total lipid content.

5. The process according to claims 2 to 3, wherein, in the seed of the transgenic plant, the docosahexaenoic acid content amounts to at least 1% by weight based on the total lipid content.

6. The process according to claims 1 to 5, wherein the nucleic acid sequences

which encode polypeptides with Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-desaturase activity are selected from the group consisting of

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201, or

b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequences shown in SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202, or

c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23, SEQ ID NO: 25, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 33, SEQ ID NO: 35, SEQ ID NO: 37, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 43, SEQ ID NO: 45, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 69, SEQ ID NO: 71, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 81, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 89, SEQ ID NO: 91, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 99, SEQ ID NO: 101, SEQ ID NO: 103, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137, SEQ ID NO: 183, SEQ ID NO: 193, SEQ ID NO: 197, SEQ ID NO: 199 or SEQ ID NO: 201, which encode polypeptides with at least 40% identity at the amino acid level with SEQ ID NO: 2, SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 8, SEQ ID NO: 10, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24, SEQ ID NO: 26, SEQ ID NO: 28, SEQ ID NO: 30, SEQ ID NO: 32, SEQ ID NO: 34, SEQ ID NO: 36, SEQ ID NO: 38, SEQ ID NO: 40, SEQ ID NO: 42, SEQ ID NO: 44, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 70, SEQ ID NO: 72, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 82, SEQ ID NO: 84, SEQ ID NO: 86, SEQ ID NO: 88, SEQ ID NO: 92, SEQ ID NO: 94, SEQ ID NO: 96, SEQ ID NO: 98, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 104, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138, SEQ ID NO: 184, SEQ ID NO: 194, SEQ ID NO: 198, SEQ ID NO: 200 or SEQ ID NO: 202 and which have Δ9-elongase, Δ6-desaturase, Δ8-desaturase, Δ6-elongase, Δ5-desaturase, Δ5-elongase or Δ4-desaturase activity.

7. The process according to claims 1 to 6, wherein a nucleic acid sequence which encodes polypeptides with ω3-desaturase activity, selected from the group

consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, or

b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 88 or SEQ ID NO: 106, or

c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 87 or SEQ ID NO: 105, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 88 or SEQ ID NO: 106 and which have ω3-desaturase activity

is additionally introduced into the transgenic plant.

8. The process according to claims 1 to 7, wherein a nucleic acid sequence which encodes polypeptides with Δ12-desaturase activity, selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, or

b) nucleic acid sequences which, as the result of the degeneracy of the genetic code, can be derived from the amino acid sequence shown in SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196, or

c) derivatives of the nucleic acid sequence shown in SEQ ID NO: 107, SEQ ID NO: 109 or SEQ ID NO: 195, which encode polypeptides with at least 60% identity at the amino acid level with SEQ ID NO: 108, SEQ ID NO: 110 or SEQ ID NO: 196 and which have Δ12-desaturase activity

is additionally introduced into the transgenic plant.

9. The process according to claims 1 to 8, wherein a nucleic acid sequence which encodes proteins of the biosynthetic pathway of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid

acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s) is additionally introduced into the transgenic plant.

10. The process according to claims 1 to 9, wherein the substituents R^2 or R^3 independently of one another are saturated or unsaturated C_{18}-C_{22}-alkylcarbonyl.

11. The process according to claims 1 to 10, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18}-, C_{20}- or C_{22}-alkylcarbonyl with at least two double bonds.

12. The process according to claims 1 to 11, wherein the transgenic plant is selected from the group of an oil-producing plant, a vegetable plant or an ornamental.

13. The process according to claims 1 to 12, wherein the transgenic organism is a transgenic plant selected from the group of the plant families: Anacardiaceae, Asteraceae, Boraginaceae, Brassicaceae, Cannabaceae, Compositae, Cruciferae, Cucurbitaceae, Elaeagnaceae, Euphorbiaceae, Fabaceae, Geraniaceae, Gramineae, Leguminosae, Linaceae, Malvaceae, Moringaceae, Marchantiaceae, Onagraceae, Olacaceae, Oleaceae, Papaveraceae, Piperaceae, Pedaliaceae, Poaceae or Solanaceae.

14. The process according to claims 1 to 13, wherein the compounds of the general formula I are isolated from the organism in the form of their oils, lipids or free fatty acids.

15. A process for the production, in transgenic plants, of compounds of the general formula I according to claim 1, comprising:

a) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a Δ6-desaturase activity and is selected from the group consisting of:

i) a nucleic acid sequence with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201,

ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 194 or SEQ ID NO: 202,

iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201, and

iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 193 or SEQ ID NO: 201,

b) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a Δ6-elongase activity and is selected from the group consisting of:

i) a nucleic acid sequence with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199,

ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 28 or SEQ ID NO: 200,

iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199, and

iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 27 or SEQ ID NO: 199, and

c) introducing, into a plant, at least one nucleic acid sequence which encodes a polypeptide with a Δ5-desaturase activity and is selected from the group consisting of:

i) a nucleic acid sequence with the sequence shown in SEQ ID NO: 11,

ii) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 12,

iii) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 11, and

iv) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 11,

where the variables and substituents in formula I have the meaning given in

claim 1.

16. The process according to claim 15, where the substituents R^2 or R^3 independently of one another are saturated or unsaturated C_{10}-C_{22}-alkylcarbonyl.

17. The process according to claim 15 or 16, wherein the substituents R^2 or R^3 independently of one another are unsaturated C_{18}-, C_{20}- or C_{22}-alkylcarbonyl with at least two double bonds.

18. The process according to claims 15 to 17, wherein a nucleic acid sequence which encodes a polypeptide with a Δ12-desaturase activity is additionally introduced into the plant.

19. The process according to claim 18, wherein the nucleic acid sequence is selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 195,

b) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 196,

c) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 195, and

d) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 195.

20. The process according to claim 18, wherein the Δ12-desaturase is expressed under the control of a seed-specific promoter.

21. The process according to claims 15 to 20, wherein a nucleic acid sequence which encodes a polypeptide with a Δ5-elongase activity is additionally introduced into the plant.

22. The process according to claim 21, wherein the nucleic acid sequence is selected from the group consisting of:

a) a nucleic acid sequence with the sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197,

b) nucleic acid sequences which encode the amino acid sequence shown in SEQ ID NO: 44, SEQ ID NO: 48, SEQ ID NO: 50, SEQ ID NO: 52, SEQ ID NO: 54, SEQ ID NO: 60, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 66, SEQ ID NO: 68, SEQ ID NO: 76, SEQ ID NO: 78, SEQ ID NO: 80, SEQ ID NO: 81, SEQ ID NO: 86, SEQ ID NO: 114, SEQ ID NO: 118, SEQ ID NO: 120, SEQ ID NO: 132, SEQ ID NO: 134, SEQ ID NO: 136, SEQ ID NO: 138 or SEQ ID NO: 198,

c) nucleic acid sequences which hybridize under stringent conditions with the complementary strand of the nucleic acid sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197, and

d) nucleic acid sequences which have at least 60% identity with the sequence shown in SEQ ID NO: 43, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 51, SEQ ID NO: 53, SEQ ID NO: 59, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 75, SEQ ID NO: 77, SEQ ID NO: 79, SEQ ID NO: 83, SEQ ID NO: 85, SEQ ID NO: 113, SEQ ID NO: 117, SEQ ID NO: 119, SEQ ID NO: 131, SEQ ID NO: 133, SEQ ID NO: 135, SEQ ID NO: 137 or SEQ ID NO: 197.

23. The process according to claim 21, wherein the Δ5-elongase is expressed under the control of a seed-specific promoter.

24. The process according to claims 12 to 24, wherein all nucleic acid sequences

are introduced into the plants on a shared recombinant nucleic acid molecule.

25. The process according to claim 24, wherein each nucleic acid sequence is under the control of its own promoter.

26. The process according to claim 25, wherein the own promoter is a seed-specific promoter.

27. The process according to claims 15 to 26, wherein, in formula I, m = 4, n = 3, p = 3 and the compound is arachidonic acid and/or m = 5, n = 3, p = 0 and the compound is eicosapentaenoic acid and/or m = 6, n = 3, p = 0 and the compound is docosahexanoic acid.

28. The process according to claims 15 to 27, wherein the plant is an oil seed plant or oil fruit plant.

29. The process according to claim 28, wherein the plant is selected from the group consisting of soybean, peanut, oilseed rape, canola, linseed, evening primrose, mullein, thistle, hazelnut, almond, macadamia, avocado, bay, wild roses, pumpkin/squash, pistachios, sesame, sunflower, safflower, borage, maize, poppy, mustard, hemp, castor-oil plant, olive, Calendula, Punica, oil palm, walnut and coconut.

30. The process according to claim 28 or 29, wherein the plant is *Brassica juncea*.

31. The process according to claims 15 to 30, wherein the compounds of the formula I are obtained from the plant in the form of their oils, lipids and free fatty acids.

32. The process according to claim 31, wherein unsaturated or saturated fatty acids are liberated from the compounds of the formula I.

33. The process according to claim 32, wherein the liberation is effected by alkaline hydrolysis or enzymatic cleavage.

34. The process according to claims 15 to 33, wherein the arachidonic acid concentration amounts to at least 25% based on the total lipid content of the transgenic plant.

35. The process according to claims 15 to 33, wherein the eicosapentaenoic acid concentration amounts to at least 15% based on the total lipid content of the transgenic plant.

36. An oil, lipid or fatty acid or a fraction thereof, obtained by a process according to one of the preceding claims.

37. The use of a Δ12-elongase, a Δ6-desaturase, a Δ5-desaturase, a Δ6-elongase and Δ5-elongase as defined in claim 15, 18 or 21, for the production of compounds of the formula I according to claim 1.

38. A recombinant nucleic acid molecule comprising:

a) one or more copies of a promoter which is active in plant cells, preferably in seed cells,
b) at least one nucleic acid sequence as defined in claim 15 which encodes a Δ6-desaturase activity,
c) at least one nucleic acid sequence as defined in claim 15 which encodes a Δ5-desaturase activity,
d) at least one nucleic acid sequence as defined in claim 15 which encodes a Δ6-elongase activity, and
e) one or more copies of a terminator sequence.

39. The recombinant nucleic acid molecule according to claim 38, additionally comprising a nucleic acid sequence as defined in claim 18 which encodes a Δ12-desaturase.

40. The recombinant nucleic acid molecule according to claim 38 or 39, additionally comprising a nucleic acid sequence as defined in claim 21 which encodes a Δ5-elongase.

41. The recombinant nucleic acid molecule according to claims 38 to 40, additionally comprising biosynthesis genes of the fatty acid or lipid metabolism selected from the group consisting of acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-

coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases and fatty acid elongase(s).

42. The recombinant nucleic acid molecule according to any of claims 38 to 41, additionally comprising biosynthesis genes of the fatty acid or lipid metabolism, selected from the group consisting of Δ4-desaturase, Δ8-desaturase, Δ9-desaturase or Δ9-elongase.

43. A transgenic plant comprising a recombinant nucleic acid molecule according to any of claims 38 to 42 or comprising the nucleic acid sequences defined in claim 15 and, if appropriate, additionally those defined in claim 18 or 21.

44. The process according to claims 15 to 35, wherein the compounds of the general formula I are isolated from the organism in the form of their oils, lipids or free fatty acids.

45. An oil, lipid or fatty acid or a fraction thereof, produced by the process according to any of claims 15 to 35.

46. An oil, lipid or fatty acid composition which comprises PUFAs produced by a process according to any of claims 1 to 14 and which is derived from transgenic plants.

47. A process for the production of oils, lipids or fatty acid compositions by mixing oils, lipids or fatty acids according to claim 45 or oil, lipid or fatty acid compositions according to claim 46 with animal or microbial oils, lipids or fatty acids.

48. The use of oils, lipids or fatty acids according to claim 45 or oil, lipid or fatty acid compositions according to claim 46 or oils, lipids or fatty acid compositions produced according to claim 46 in feed, foodstuffs, cosmetics or pharmaceuticals.

49. An isolated nucleic acid sequence which encodes polypeptides with Δ5-elongase activity and which has the sequence shown in SEQ ID NO: 197.

50. An isolated nucleic acid sequence which encodes polypeptides with Δ6-

elongase activity and which has the sequence shown in SEQ ID NO: 199.

51. An isolated nucleic acid sequence which encodes polypeptides with Δ6-desaturase activity and which has the sequence shown in SEQ ID NO: 201.

52. A gene construct comprising an isolated nucleic acid according to any of claims 49 to 51, wherein the nucleic acid is linked functionally to one or more regulatory signals.

53. The gene construct according to claim 53, wherein the nucleic acid construct comprises additional biosynthesis genes of the fatty acid or lipid metabolism selected from the group acyl-CoA dehydrogenase(s), acyl-ACP [= acyl carrier protein] desaturase(s), acyl-ACP thioesterase(s), fatty acid acyltransferase(s), acyl-CoA:lysophospholipid acyltransferase(s), fatty acid synthase(s), fatty acid hydroxylase(s), acetyl-coenzyme A carboxylase(s), acyl-coenzyme A oxidase(s), fatty acid desaturase(s), fatty acid acetylenases, lipoxygenases, triacylglycerol lipases, allenoxide synthases, hydroperoxide lyases or fatty acid elongase(s).

54. A vector comprising a nucleic acid according to claim 50 or 51 or a gene construct according to claim 52 or 53.

55. A transgenic plant comprising at least one nucleic acid according to claim 50 or 51 or a gene construct according to claim 52 or 53 or a vector according to claim 54.